

5 (i) APPLICANT: GOEDDEL, DAVID V.
ROTHE, MIKE

10 (iii) NUMBER OF SEQUENCES: 8

(A) ADDRESSEE: Genentech, Inc.

(C) CITY: South San Francisco

(E) COUNTRY: USA

(F) ZIP: 94080

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: WinPatin (Genentech)

(A) APPLICATION NUMBER:

(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

5 (A) APPLICATION NUMBER: 60/002382
(B) FILING DATE: 17-aug-1995

(viii) ATTORNEY/AGENT INFORMATION:

10 (A) NAME: Dreger, Ginger R.
(B) REGISTRATION NUMBER: 33,055
(C) REFERENCE/DOCKET NUMBER: P0960R1D1

(ix) TELECOMMUNICATION INFORMATION:

15 (A) TELEPHONE: 650/225-3216
(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 413 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

25 Met Asp Lys Asn Ile Gly Glu Gln Leu Asn Arg Ala Tyr Glu Ala
1 5 10 15

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Phe Arg Gln Ala Cys Met Asp Arg Asp Ser Ala Val Arg Glu Leu
20 25 30

Gln Gln Lys Thr Glu Asn Tyr Glu Gln Arg Ile Arg Glu Gln Gln
5 35 40 45

Glu Gln Leu Ser Phe Gln Gln Asn Leu Ile Asp Arg Leu Lys Ser
50 55 60

Gln Leu Leu Leu Val Asp Ser Ser Arg Asp Asn Ser Tyr Gly Tyr
10 65 70 75

Val Pro Leu Leu Glu Asp Ser Asp Arg Arg Lys Asn Asn Leu Thr
80 85 90

Leu Asp Glu Pro His Asp Lys Val Lys Leu Gly Thr Leu Arg Asp
15 95 100 105

Lys Gln Ser Lys Val Arg Arg Gln Glu Val Ser Ser Gly Lys Glu
20 110 115 120

Ser Ala Lys Gly Leu Asn Ile Pro Leu His His Glu Arg Asp Asn
125 130 135

Ile Glu Lys Thr Phe Trp Asp Leu Lys Glu Glu Phe His Arg Ile
25 140 145 150

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Cys Leu Leu Ala Lys Ala Gln Lys Asp His Leu Ser Lys Leu Asn
155 160 165

Ile Pro Asp Ile Ala Thr Asp Thr Gln Cys Ser Val Pro Ile Gln
5 170 175 180

Cys Thr Asp Lys Thr Glu Lys Gln Glu Ala Leu Phe Lys Pro Gln
185 190 195

Ala Lys Asp Asp Ile Asn Arg Gly Met Ser Cys Val Thr Ala Val
10 200 205 210

Thr Pro Arg Gly Leu Gly Arg Asp Glu Glu Asp Thr Ser Phe Glu
215 220 225

Ser Leu Ser Lys Phe Asn Val Lys Phe Pro Pro Met Asp Asn Asp
15 230 235 240

Ser Ile Phe Leu His Ser Thr Pro Glu Ala Pro Ser Ile Leu Ala
20 245 250 255

Pro Ala Thr Pro Glu Thr Val Cys Gln Asp Arg Phe Asn Met Glu
260 265 270

Val Arg Asp Asn Pro Gly Asn Phe Val Lys Thr Glu Glu Thr Leu
25 275 280 285

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Phe Glu Ile Gln Gly Ile Asp Pro Ile Thr Ser Ala Ile Gln Asn
 290 295 300

Leu Lys Thr Thr Asp Lys Thr Asn Pro Ser Asn Leu Arg Ala Thr
 5 305 310 315

Cys Leu Pro Ala Gly Asp His Asn Val Phe Tyr Val Asn Thr Phe
 320 325 330

Pro Leu Gln Asp Pro Pro Asp Ala Pro Phe Pro Ser Leu Asp Ser
 10 335 340 345

Pro Gly Lys Ala Val Arg Gly Pro Gln Gln Pro Phe Trp Lys Pro
 350 355 360

Phe Leu Asn Gln Asp Thr Asp Leu Val Val Pro Ser Asp Ser Asp
 15 365 370 375

Ser Glu Leu Leu Lys Pro Leu Val Cys Glu Phe Cys Gln Glu Leu
 20 380 385 390

Phe Pro Pro Ser Ile Thr Ser Arg Gly Asp Phe Leu Arg His Leu
 395 400 405

Asn Thr His Phe Asn Gly Glu Thr
 25 410 413

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1955 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTGGAACGGA AAGCTACTTC CGGTTGCAGT CATTCTGCCG GGCACCGGCG 50
ACCTGTGGCG TGAGCGAGCA CAGCCGGAAC CCTCCACTAG CTGGCATTCC 100
TACCATCCTT TATAGTGATG CTACAGGACA AAGAGGAATG GATAAAAACA 150
TTGGTGAGCA ACTCAATAGA GCATATGAAG CCTTCCGACA GGCATGCATG 200
GATAGAGATT CAGCAGTAAG AGAGCTACAG CAAAAGCAGA CTGAGAACTA 250
TGAACAAAGA ATACGCGAGC AACAGGAACA GCTGTCATTT CAACAAAACC 300
TAATTGACAG GCTGAAATCA CAGCTACTTC TCGTGGATTC TAGTCGAGAT 350
AACAGTTATG GCTATGTACC TTTGCTTGAA GACAGTGACA GAAGGAAGAA 400

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TAATTTGACC CTTGATGAAC CACATGATAA AGTGAAACTA GGAACACTGA 450

GAGATAAGCA ATCAAAGGTG AGACGACAAG AAGTTTCTTC TGGAAAAGAA 500

5 TCCGCCAAGG GTCTCAACAT CCCTCTGCAT CACGAAAGGG ATAATATAGA 550

GAAGACTTTC TGGGACCTTA AAGAAGAATT TCATAGGATT TGCTTGCTAG 600

CAAAAGCACA GAAAGATCAC TTAAGCAAAC TTAATATACC AGATATTGCA 650

10

ACTGACACAC AGTGTTCTGT GCCTATACAG TGTACTGATA AAACAGAGAA 700

ACAAGAAGCG CTGTTTAAGC CCCAGGCTAA AGATGATATA AATAGAGGTA 750

15

TGTCGTGCGT CACAGCTGTC ACACCAAGAG GACTGGGCCG GGATGAGGAA 800

GATACCTCTT TTGAATCACT TTCTAAATTC AATGTCAAGT TTCCGCCTAT 850

GGACAATGAC TCTATTTTTC TACATAGCAC TCCAGAGGCC CCGAGCATCC 900

20

TTGCTCCTGC CACACCTGAG ACAGTGTGCC AGGACCGATT TAATATGGAA 950

GTCAGAGACA ACCCAGGAAA CTTTGTTAAA ACAGAAGAAA CTTTATTGTA 1000

25

AATTCAGGGA ATTGACCCCA TAACTTCAGC TATACAAAAC CTAAAACAA 1050

CTGACAAAAC AAACCCCTCA AATCTTAGAG CGACGTGTTT GCCAGCTGGA 1100

PATENT DOCKET P0960R1D1

GACCACAATG TGTTCTATGT AAATACGTTT CCACTTCAAG ACCCGCCTGA 1150

CGCACCTTTT CCCTCACTGG ATTCCCCAGG AAAGGCTGTC CGAGGACCAC 1200

5 AGCAGCCCTT TTGGAAGCCT TTTCTTAACC AAGACACTGA CTTAGTGGTA 1250

CCAAGTGATT CAGACTCAGA GCTCCTTAAA CCTCTAGTGT GTGAATTCTG 1300

TCAAGAGCTT TTCCCACCAT CCATTACATC CAGAGGGGAT TTCCTCCGGC 1350

10 ATCTTAATAC AACTTTAAT GGGGAGACTT AAATCACGTT TGAAAACAGA 1400

CATATCATGT TCTCTGTGGT GGTTTTGGAT TTGTAACGCT AGAGAACGCT 1450

15 TTCTCGTGAG CCAAATGTAA GATTGATTAT AAAGTTGTTA CTTTATCTTT 1500

TAAGAGATCA TTTTGTATAG AACTATAACT CATTATATTA TTCATGTTTA 1550

TACCTATAAT TTCTACATTT CAAAATTACA CATGTGACTT ACAGAGTTAT 1600

20 TCAGTCATAA TTTATGTTTC AAATAGCTAA GTTTATTGTT TGACTATTGT 1650

GAGATCTATT AAATTTAGTA ATAGCAAATG TTTATAGGAT ATTCAAATTT 1700

25 CATTTGAATT TTTAATTATT TTTGCTACAG GTAATATTCC TTTAAAATAC 1750

GTATATAACG TACAGAGAAT AACAGACAAT ATGATCTAAG TAAATGTCGA 1800

ATCAATCATT AGTTGCCCAG GGAAATTTAA ACATTATAGA TCATTTTTAA 1850

ATAATACACA TAGTTTTAAT TTTTACTGTG TGTATAGATG CATGATTAAA 1900

5 TGACTIONTAAAT ATTAAAAGTG ACTTACGTCG TGCTTATTAA AAAAAAAAAA 1950

AAAAA 1955

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ser	Leu	Lys	Arg	His	Ser	Leu	Arg	Arg	Asn	Ala	Cys	His	Leu
1				5				10					15	

Glu	Thr	Arg	Ala	Gly	Ile	Pro	Thr	Ile	Leu	Tyr	Ser	Asp	Ala	Thr
				20				25					30	

Gly Gln Arg Gly

34

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCACGCGTC CGGTTTGGGC AGCATCTGTA GAGCCTGTGC AAACGGCTTC 50
CAGAATGGGT ACGTGCCTAT GTCTTTAAAG AGACATAGTC TGCGAAGGAA 100
CGCCTGTCAC CTGGAGACGA GAGCTGGCAT TCCTACCATC CTTTATAGTG 150
ATGCTACAGG ACAAAGAGGA 170

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asp Lys Asn Ile Gly Glu Gln Leu Asn Lys Ala Tyr Glu Ala
1 5 10 15

Phe Arg Gln Ala Cys Met Asp Arg Asp Ser Ala Val Lys Glu Leu
20 25 30

Gln Gln Lys Thr Glu Asn Tyr Glu Gln Arg Ile Arg Glu Gln Gln
35 40 45

Glu Gln Leu Ser Leu Gln Gln Thr Ile Ile Asp Lys Leu Lys Ser
50 55 60

Gln Leu Leu Leu Val Asn Ser Thr Gln Asp Asn Asn Tyr Gly Cys
65 70 75

Val Pro Leu Leu Glu Asp Ser Asp Thr Arg Lys Asn Thr Leu Thr
80 85 90

Leu Ala Gln Pro Gln Asp Lys Val Ile Ser Gly Ile Ala Arg Glu
95 100 105

Lys Leu Pro Lys Val Arg Arg Gln Glu Val Ser Ser Pro Arg Lys
110 115 120

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Glu Thr Ser Ala Arg Ser Leu Gly Ser Pro Leu Leu His Glu Arg
 125 130 135

Gly Asn Ile Glu Lys Thr Ser Trp Asp Leu Lys Glu Glu Phe His
 140 145 150

Lys Ile Cys Met Leu Ala Lys Ala Gln Lys Asp His Leu Ser Lys
 155 160 165

Leu Asn Ile Pro Asp Thr Ala Thr Glu Thr Gln Cys Ser Val Pro
 170 175 180

Ile Gln Cys Thr Asp Lys Thr Asp Lys Gln Glu Ala Leu Phe Thr
 185 190 195

Pro Gln Ala Lys Asp Asp Ile Asn Arg Gly Ala Pro Ser Ile Thr
 200 205 210

Ser Val Thr Pro Arg Gly Leu Cys Arg Asp Glu Glu Asp Thr Ser
 215 220 225

Leu Glu Ser Leu Ser Lys Phe Asn Val Lys Phe Pro Pro Met Asp
 230 235 240

Asn Asp Ser Thr Phe Leu His Ser Thr Pro Glu Arg Pro Gly Ile
 245 250 255

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Leu Ser Pro Ala Thr Ser Glu Ala Val Cys Gln Glu Lys Phe Asn
260 265 270

Met Glu Phe Arg Asp Asn Pro Gly Asn Phe Val Lys Thr Glu Glu
5 275 280 285

Thr Leu Phe Glu Ile Gln Gly Ile Asp Pro Ile Ala Ser Ala Ile
290 295 300

Gln Asn Leu Lys Thr Thr Asp Lys Thr Lys Pro Ser Asn Leu Val
10 305 310 315

Asn Thr Cys Ile Arg Thr Thr Leu Asp Arg Ala Ala Cys Leu Pro
320 325 330

Pro Gly Asp His Asn Ala Leu Tyr Val Asn Ser Phe Pro Leu Leu
335 340 345

Asp Pro Ser Asp Ala Pro Phe Pro Ser Leu Asp Ser Pro Gly Lys
20 350 355 360

Ala Ile Arg Gly Pro Gln Gln Pro Ile Trp Lys Pro Phe Pro Asn
365 370 375

Gln Asp Ser Asp Ser Val Val Leu Ser Gly Thr Asp Ser Glu Leu
25 380 385 390

His Ile Pro Arg Val Cys Glu Phe Cys Gln Ala Val Phe Pro Pro
 395 400 405

5 Ser Ile Thr Ser Arg Gly Asp Phe Leu Arg His Leu Asn Ser His
 410 415 420

Phe Asn Gly Glu Thr
 425

10 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2108 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTTGAGCAG CATTGTTAGA GCCTGTGGAA AACACTTTAC AACTGTGTAA 50

CTGTCTTCAT CTTTACAGAG GAATAGTCTA CAAAGGAAGA CTTGTAACCT 100

25 GGAGAAGAGA CCTGTCATTT ACTCCATCCT TTATAGTGAT GCTACAGGAC 150

GAAGAGGAAT GGATAAAAAC ATTGGCGAGC AACTCAATAA AGCGTATGAA 200

GCCTTCCGGC AGGCATGCAT GGATAGAGAT TCTGCAGTAA AAGAATTACA 250

GCAAAAGACT GAGAACTATG AGCAGAGAAT ACGTGAACAA CAGGAACAGC 300

5 TGTCACTCCA ACAGACTATT ATTGACAAGC TAAAATCTCA GTTACTTCTT 350

GTGAATTCCA CTCAAGATAA CAATTATGGC TGTGTCCCTC TGCTTGAAGA 400

CAGTGACACA AGAAAGAATA CTTTGACTCT TGCTCAGCCA CAAGATAAAG 450

10

TGATTTTCAGG AATAGCAAGA GAAAACTAC CAAAGGTAAG AAGACAAGAG 500

GTTTCTTCTC CTAGAAAAGA AACTTCAGCA AGGAGTCTTG GCAGTCCTTT 550

15

GCTCCATGAA AGGGGTAATA TAGAGAAGAC TTCCTGGGAT CTGAAAGAAG 600

AATTTCATAA AATATGCATG CTAGCAAAAG CACAGAAAGA CCACTTAAGC 650

AAACTTAATA TACCAGACAC TGCAACTGAA ACACAGTGCT CTGTGCCTAT 700

20

ACAGTGTACG GATAAAACAG ATAAACAAGA AGCGCTGTTT ACGCCTCAGG 750

CTAAAGATGA TATAAATAGA GGTGCACCAT CCATCACATC TGTCACACCA 800

25

AGAGGACTGT GCAGAGATGA GGAAGACACC TCTTTGGAAT CACTTTCTAA 850

ATTCAATGTC AAGTTTCCAC CTATGGACAA TGA CTCAACT TTCTTACATA 900

PATENT DOCKET P0960R1D1

GCACTCCAGA GAGACCCGGC ATCCTTAGTC CTGCCACGTC TGAGGCAGTG 950

TGCCAAGAGA AATTTAATAT GGAGTTCAGA GACAACCCAG GGAACCTTGT 1000

5 TAAAACAGAA GAAACTTTAT TTGAAATTCA GGGAATTGAC CCCATAGCTT 1050

CAGCTATACA AAACCTTAAA ACAACTGACA AAACAAAGCC CTCAAATCTC 1100

GTAAACACTT GTATCAGGAC AACTCTGGAT AGAGCTGCGT GTTTGCCACC 1150

10 TGGAGACCAT AATGCATTAT ATGTAAATAG CTTCCCACTT CTGGACCCAT 1200

CTGATGCACC TTTTCCCTCA CTCGATTCCC CGGGAAAAGC AATCCGAGGA 1250

15 CCACAGCAGC CCATTTGGAA GCCCTTTCCT AATCAAGACA GTGACTCGGT 1300

GGTACTAAGT GGCACAGACT CAGAACTGCA TATACCTCGA GTATGTGAAT 1350

TCTGTCAAGC AGTTTTCCCA CCATCCATTA CATCCAGGGG GGATTTTCCTT 1400

20 CGGCATCTTA ATTCACACTT CAATGGAGAG ACTTAAGACA CATTTGAAAA 1450

CAGACATATC AAGTTCTATG TGATGATTTT GGGTTTTTAA TACTATAAAT 1500

25 ACTTGATTGT AAATAAATT CAAGATCATT TATAGGAAAA TCTAGTTTCA 1550

CAGCTATTTG AATTTTTTTC TGGATTACT ATATAACTCT TATTTTTTAA 1600

AAGATCATTC TGTTCCTTCA AGGAGAAATA AGCCTAAAAG AAGAAAAACA 1650

AAAAAATTC TGTATAAAC TGTAATCCTT TGTATTCATG TTTACAGTGC 1700

5 TATTACTATA ATTCAAAATT ATGTATGTGA CTTAGAGTTA TATAATCATA 1750

ATTTATGTTT ATTTCAAATA TCTAAGTTTA TTGCTTGGAT TTCTAGTGAG 1800

AGCTGTTGAA TTTGGTGATG TCAAATGTTT CTAGGGTTTT TTAGTTTGTT 1850

10

TTTATTGAGA AAATTGATTA TTTATGCTAT AGGTGATATT CTCTTTGAAT 1900

AAACCTATAA TAGGAAATAG CAGACCACAT AACATCTTT GTAAATATCA 1950

15

AACCTAATAC ATTTCTTGTC CAGTGATAAA ACAACTGGTA GAATTATTTA 2000

AACACTTTAG ATTTTTAAAT AATAAACATG GCTTTAATTT TTAGTGTTG 2050

TATAGCTACA TGATGAAATT AATTAAATAT TAAGAGGTAA AAAAAAAAAA 2100

20

AAAAAAAA 2108

(2) INFORMATION FOR SEQ ID NO:7:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1922 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5

CGGAAAGCTA CTTCCGGTTG CAGTCATTCT GCCGGGCACC GGCGACCTGT 50

GGCGTGAGCG AGCACAGCCG GAACCCTCCA CTAGCTGGCA TTCCTACCAT 100

10

CCTTTATAGT GATGCTACAG GACAAAGAGG AATGGATAAA AACATTGGTG 150

AGCAACTCAA TAGAGCATAT GAAGCCTTCC GACAGGCATG CATGGATAGA 200

15

GATTCAGCAG TAAGAGAGCT ACAGCAAAAG CAGACTGAGA ACTATGAACA 250

AAGAATACGC GAGCAACAGG AACAGCTGTC ATTTCAACAA AACCTAATTG 300

ACAGGCTGAA ATCACAGCTA CTTCTCGTGG ATTCTAGTCG AGATAACAGT 350

20

TATGGCTATG TACCTTTGCT TGAAGACAGT GACAGAAGGA AGAATAATTT 400

GACCCTTGAT GAACCACATG ATAAAGTGAA ACTAGGAACA CTGAGAGATA 450

25

AGCAATCAAA GGTGAGACGA CAAGAAGTTT CTTCTGGAAA AGAATCCGCC 500

AAGGGTCTCA ACATCCCTCT GCATCACGAA AGGGATAATA TAGAGAAGAC 550

TTTCTGGGAC CTTAAAGAAG AATTTCATAG GATTGCTTG CTAGCAAAAG 600

CACAGAAAGA TCACTTAAGC AACTTAATA TACCAGATAT TGCAACTGAC 650

5 ACACAGTGTT CTGTGCCTAT ACAGTGTACT GATAAAACAG AGAAACAAGA 700

AGCGCTGTTT AAGCCCCAGG CTAAAGATGA TATAAATAGA GGTATGTCGT 750

GCGTCACAGC TGTCACACCA AGAGGACTGG GCCGGGATGA GGAAGATACC 800

10 TCTTTTGAAT CACTTTCTAA ATTCAATGTC AAGTTTCCGC CTATGGACAA 850

TGACTCTATT TTTCTACATA GCACTCCAGA GGCCCCGAGC ATCCTTGCTC 900

15 CTGCCACACC TGAGACAGTG TGCCAGGACC GATTTAATAT GGAAGTCAGA 950

GACAACCCAG GAAACTTTGT TAAAACAGAA GAACTTTAT TTGAAATTCA 1000

GGGAATTGAC CCCATAACTT CAGCTATACA AAACCTTAAA ACAACTGACA 1050

20 AAACAAACCC CTCAAATCTT AGAGCGACGT GTTTGCCAGC TGGAGACCAC 1100

AATGTGTTCT ATGTAAATAC GTTCCCACTT CAAGACCCGC CTGACGCACC 1150

25 TTTTCCCTCA CTGGATTCCC CAGGAAAGGC TGTCCGAGGA CCACAGCAGC 1200

CCTTTTGGAA GCCTTTTCTT AACCAAGACA CTGACTTAGT GGTACCAAGT 1250

GATTCAGACT CAGAGCTCCT TAAACCTCTA GTGTGTGAAT TCTGTCAAGA 1300

GCTTTTCCCA CCATCCATTA CATCCAGAGG GGATTTCCTC CGGCATCTTA 1350

5 ATACACACTT TAATGGGGAG ACTTAAATCA CGTTTGAAAA CAGACATATC 1400

ATGTTCTCTG TGGTGGTTTT GGATTGTAA CGCTAGAGAA CGCTTCTCG 1450

TGAGCCAAAT GTAAGATTGA TTATAAAGTT GTTACTTTAT CTTTAAAGAG 1500

10

ATCATTTTGT ATAGAACTAT AACTCATTAT ATTATTCATG TTTATACCTA 1550

TAATTTCTAC ATTTCAAAT TACACATGTG ACTTACAGAG TTATTCAGTC 1600

15

ATAATTTATG TTTCAAATAG CTAAGTTTAT TGTTTGACTA TTGTGAGATC 1650

TATTAAATTT AGTAATAGCA AATGTTTATA GGATATTCAA ATTTCATTTG 1700

AATTTTAAAT TATTTTGTCT ACAGGTAATA TTCCTTTAAA ATACGTATAT 1750

20

AACGTACAGA GAATAACAGA CAATATGATC TAAGTAAATG TCGAATCAAT 1800

CATTAGTTGC CCAGGGAAAT TTAAACATTA TAGATCATTT TTAAATAATA 1850

25 CACATAGTTT TAATTTTAC TGTGTGTATA GATGCATGAT TAAATGACTT 1900

AAATATTAAA AAAAAAAAAA AA 1922

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2160 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGCGACCTG TGGCGTGAGC GAGCACAGCC GGAACCCTCC ACTAGCTGGC 50
ATTCCTACCA TCCTTTATAG TGATGCTACA GGACAAAGAG GAATGGATAA 100
AAACATTGGT GAGCAACTCA ATAGAGCATA TGAAGCCTTC CGACAGGCAT 150
GCATGGATAG AGATTCAGCA GTAAGAGAGC TACAGCAAAA GACTGAGAAC 200
TATGAACAAA GAATACGCGA GCAACAGGAA CAGCTGTCAT TTCAACAAAA 250
CCTAATTGAC AGGCTGAAAT CACAGCTACT TCTCGTGGAT TCTAGTCGAG 300
ATAACAGTTA TGGCTATGTA CCTTTGCTTG AAGACAGTGA CAGAAGGAAG 350
AATAATTTGA CCCTTGATGA ACCACATGAT AAAGTGAAAC TAGGAACACT 400

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GAGAGATAAG CAATCAAAGG TGAGACGACA AGAAGTTTCT TCTGGAAAAG 450

AATCCGCCAA GGGTCTCAAC ATCCCTCTGC ATCACGAAAG GGATAATATA 500

5 GAGAAGACTT TCTGGGACCT TAAAGAAGAA TTTCATAGGA TTTGCTTGCT 550

AGCAAAAGCA CAGAAAGATC ACTTAAGCAA ACTTAATATA CCAGATATTG 600

CAACTGACAC ACAGTGTTCT GTGCCTATAC AGTGTAAGTA TAAACAGAG 650

10

AAACAAGAAG CGCTGTTTAA GCCCCAGGCT AAAGATGATA TAAATAGAGG 700

TATGTCGTGC GTCACAGCTG TCACACCAAG AGGACTGGGC CGGGATGAGG 750

15

AAGATACCTC TTTTGAATCA CTTTCTAAAT TCAATGTCAA GTTTCGCCT 800

ATGGACAATG ACTCTATTTT TCTACATAGC ACTCCAGAGG CCCCAGCAT 850

CCTTGCTCCT GCCACACCTG AGACAGTGTG CCAGGACCGA TTTAATATGG 900

20

AAGTCAGAGA CAACCCAGGA AACTTTGTTA AAACAGAAGA AACTTTATTT 950

GAAATTCAGG GAATTGACCC CATAACTTCA GCTATACAAA ACCTTAAAC 1000

25

AACTGACAAA ACAAACCCCT CAAATCTTAG AGCGACGTGT TTGCCAGCTG 1050

GAGACCACAA TGTGTTCTAT GTAAATACGT TCCCACTTCA AGACCCGCCT 1100

GACGCACCTT TTCCCTCACT GGATTCCCCA GGAAAGGCTG TCCGAGGACC 1150

ACAGCAGGTA ACTGTTTTGC ATTAACAAAT ATTTTATTAT GTGTGAACAC 1200

5 ACATTTTATC ATACATGTAC AGATACAAAT CTGTTTTAAG TTATCAGGCA 1250

TCCATTTAAA ATTAATGACT ATCCAGAGTT GAGGCTTTCA ATAAAATATG 1300

TAAGTTCTGT ATTCAAGGAC ATGAATTTTG AATGTGACTG CGCTAAAGCT 1350

10 TCCTTGTGAT ACTGTGGCGT GGCTTTCCTT GCTTCGTCCT CTTCAAGCAC 1400

AGCTTGTTGA CATCAGTGCT CTAATGGATG CTTTATTAAA GTCAGTTACA 1450

15 GGCAGTAAAT AATTTTTTTA AACTTGTGT AGGTACACAT AATAATGTGT 1500

AATTTTCCAT AAGTAGATAA TTGCACCAAA TATTCAAAT AACTGTTCAT 1550

TCAGCCTACT TGTGTTACAT TTCTAGTTAC AGCAGTACAG AGGTCTGTAG 1600

20 TGTTTGGTTT GTTTACTAAC CTGACACTAA GCAGATATCC TTATACAGTT 1650

TTCAAATAAT CCCTGCACAT GAATACTGTA ATCAAATCTC TTCTTTACTG 1700

25 TTTGTGAAGC ACAAAGACTT TATAGCCCAT GAATCTAATC CTACCATCCT 1750

TTCTTCCAGA TTCAGGTTCT TTCACAGAAA TATTCCTTTT TGTTAGGAAG 1800

PATENT DOCKET P0960R1D1

AAAAAAAGTT TTGTTTAATT TCTGAAGGTA AATGCTAAGT GTAGAAATGT 1850

TAAAATAAAT AGAAGCATCT CATTAGAACT TTCAAACATT TGATTTTCTA 1900

5 TCAGATTAAA AAAAATACTT AATACCTTTG GTTTACGTAT TCCTATCAGT 1950

TATAGGCTTT TTGAACAGCA TGGAAGAAG CAATAGTGAA GCTGTAGGAT 2000

GTCTTAGTAG TGGGCGTAAG TAGAGATTCT GACAAGTCTT AATTATTAAC 2050

10 TCTCTTATGT TCCACCCTGT ACCTTATTTT ACTTTATGGT CTCAGCTATA 2100

GTTGCTACCA AATGAAACAA TTAAACAATT TCATGTGTTG CGAAAAAAAA 2150

15 AAAAAAAAAA 2160